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* * * * * * * * * * * * * STN  Columbus  * * *
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FILE 'HOME' ENTERED AT 09:11:11 ON 23 AUG 2001

=> index bioscience
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
COST IN U.S. DOLLARS
SINCE FILE      TOTAL

ENTRY    SESSION
FULL ESTIMATED COST
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INDEX 'ADISALERTS, ADISINSIGHT, AGRICOLA,
ANABSTR, AQUASCI, BIOBUSINESS,
       BIOCOMMERCE, BIOSIS, BIOTECHABS,
BIOTECHDS, BIOTECHNO, CABA, CANCERLIT,
       CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI,
CROPB, CROPU, DDFB, DDFU, DGENE,
       DRUGB, DRUGLAUNCH, DRUGMONOG2, DRUGNL,
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59 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term
postings or to view
search error messages that display as 0* with
SET DETAIL OFF.

=> s aeromonas(3a)aminopeptidase
          2   FILE AGRICOLA
          1   FILE ANABSTR
          5   FILE BIOBUSINESS
         47   FILE BIOSIS
         13   FILE BIOTECHABS
         13   FILE BIOTECHDS
         25   FILE BIOTECHNO
          3   FILE CABA
          3   FILE CANCERLIT
         88   FILE CAPLUS
          2   FILE CEABA-VTB
          2   FILE CIN
          1   FILE CONFSCI
          2   FILE DDFB
          3   FILE DDFU
         55   FILE DGENE
          2   FILE DRUGB
  24 FILES SEARCHED...
          4   FILE DRUGU
          1   FILE EMBAL
         39   FILE EMBASE
         26   FILE ESBIOBASE
          4   FILE FROSTI
          9   FILE FSTA
          5   FILE GENBANK
          3   FILE IFIPAT
          5   FILE JICST-EPLUS
         30   FILE LIFESCI
         49   FILE MEDLINE
  45 FILES SEARCHED...
         14   FILE PASCAL
         64   FILE SCISEARCH
          3   FILE TOXLINE
          5   FILE TOXLIT
          9   FILE USPATFULL
          4   FILE WPIDS
          4   FILE WPINDEX

  35 FILES HAVE ONE OR MORE ANSWERS,    59
FILES SEARCHED IN STNINDEX

L1   QUE AEROMONAS(3A) AMINOPEPTIDASE

=> s l1 (l) (alanine or alanyl)
          4   FILE BIOSIS
          2   FILE BIOTECHABS
          2   FILE BIOTECHDS
          1   FILE BIOTECHNO
          6   FILE CAPLUS
  21 FILES SEARCHED...
          9   FILE DGENE
          3   FILE EMBASE
          1   FILE ESBIOBASE
  39 FILES SEARCHED...
          3   FILE LIFESCI
          4   FILE MEDLINE
          1   FILE SCISEARCH
          7   FILE USPATFULL
          1   FILE WPIDS
          1   FILE WPINDEX

  14 FILES HAVE ONE OR MORE ANSWERS,    59
FILES SEARCHED IN STNINDEX

L2   QUE L1 (L) (ALANINE OR ALANYL)

=> s l2 and py<2000
          0*  FILE ADISINSIGHT
   3 FILES SEARCHED...
          4   FILE BIOSIS
   8 FILES SEARCHED...
          1   FILE BIOTECHABS
          1   FILE BIOTECHDS
          1   FILE BIOTECHNO
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          0*  FILE FOREGE
  39 FILES SEARCHED...
          3   FILE LIFESCI
  42 FILES SEARCHED...
          0*  FILE MEDICONF
          4   FILE MEDLINE
  46 FILES SEARCHED...
  48 FILES SEARCHED...
          0*  FILE PHAR
  52 FILES SEARCHED...
          1   FILE SCISEARCH
  55 FILES SEARCHED...
          7   FILE USPATFULL
  58 FILES SEARCHED...

  11 FILES HAVE ONE OR MORE ANSWERS,    59
FILES SEARCHED IN STNINDEX

L3   QUE L2 AND PY<2000

=> d rank
F1          7   USPATFULL
F2          5   CAPLUS
F3          4   BIOSIS
F4          4   MEDLINE
F5          3   EMBASE
F6          3   LIFESCI
F7          1   BIOTECHABS
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F8              1   BIOTECHDS
F9              1   BIOTECHNO
F10             1   ESBIOBASE
F11             1   SCISEARCH


=> file f2-11
COST IN U.S. DOLLARS
SINCE FILE      TOTAL

ENTRY    SESSION
FULL ESTIMATED COST
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   4 FILES SEARCHED...
   7 FILES SEARCHED...
L4          23 L3

=> dup rem
ENTER L# LIST OR (END):l4
PROCESSING COMPLETED FOR L4
L5            7 DUP REM L4 (16 DUPLICATES
REMOVED)

                    ANSWERS '1-5' FROM FILE CAPLUS
                    ANSWER '6' FROM FILE BIOSIS
                    ANSWER '7' FROM FILE BIOTECHDS

=> d bib ab 1-7

L5   ANSWER 1 OF 7  CAPLUS  COPYRIGHT 2001 ACS
DUPLICATE 1
AN   1998:798938  CAPLUS
DN   130:121291
TI   Inhibition of Streptomyces griseus
aminopeptidase and effects of calcium
     ions on catalysis and binding.
Comparisons with the homologous enzyme
     Aeromonas proteolytica aminopeptidase
AU   Papir, Galia; Spungin-Bialik, Anya; Ben-
Meir, Daniella; Fudim, Ella;
     Gilboa, Rotem; Greenblatt, Harry M.;
Shoham, Gil; Lessel, Uta; Schomburg,
     Dietmar; Ashkenazi, Ruth; Blumberg,
Shmaryahu
CS   Sackler Institute of Molecular Medicine,
Department of Human Genetics and
     Molecular Medicine, Sackler Faculty of
Medicine, Tel Aviv University, Tel
     Aviv-Jaffa, IL-69978, Israel
SO   Eur. J. Biochem. (  ***1998***  ),
258(2), 313-319
     CODEN: EJBCAI; ISSN: 0014-2956
PB   Springer-Verlag
DT   Journal
LA   English
AB   Streptomyces griseus aminopeptidase is a
zinc metalloenzyme contg. 2 mol
     zinc/mol protein, similar to the
homologous enzyme   ***Aeromonas***
     proteolytica   ***aminopeptidase***  .
In addn., a unique Ca2+-binding
     site has been identified in the
Streptomyces enzyme, which is absent in
     the Aeromonas enzyme.  Binding of Ca2+
enhances stability of the
     Streptomyces enzyme and modulates its
activity and affinity towards
     substrates and inhibitors in a structure-
dependent manner.  Among the
     three hydrophobic 4-nitroanilides of
***alanine***  , valine and
     leucine, the latter displays the largest
overall activation (increase in
     kcat/Km).  Large enhancements in affinity
(1/Ki) upon Ca2+ binding have
     been obsd. for inhibitors with flexible
(leucine-like) residues at their
     N-termini and smaller enhancements for
inhibitors with rigid
     (phenylalanine-like) residues.
RE.CNT  25
RE
(1) Almquist, R; J Med Chem 1980, V23, P1392
CAPLUS
(2) Bayliss, M; Biochemistry 1986, V25, P8113
CAPLUS
(4) Ben-Meir, D; Eur J Biochem 1993, V212,
P107 CAPLUS
(5) Burley, S; Proc Natl Acad Sci USA 1990,
V87, P6878 CAPLUS
(6) Chevrier, B; Eur J Biochem 1996, V237,
P393 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT
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L5 ANSWER 2 OF 7 CAPLUS COPYRIGHT 2001 ACS DUPLICATE 3
AN 1987:511685 CAPLUS
DN 107:111685
TI Hydroxamate-induced spectral perturbations of cobalt Aeromonas aminopeptidase
AU Wilkes, Stella H.; Prescott, John M.
CS Coll. Med., Texas A and M Univ., College Station, TX, 77843, USA
SO J. Biol. Chem. (***1987***), 262(18), 8621-5
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB The absorption spectrum of Co(II)-substituted ***Aeromonas*** ***aminopeptidase*** is markedly perturbed by the presence of equimolar concns. of D-amino acid hydroxamates and acyl hydroxamates, powerful inhibitors of this enzyme. D-Valine hydroxamate produces the most distinctive perturbation, splitting the characteristic 527-nm absorption peak of the Co enzyme to form peaks at 564, 520, and 487 nm with molar extinction values of 126, 98, and 67 M-1 cm-1, resp. A qual. similar perturbation, albeit with lower extinction values, results from the addn. of D-leucine hydroxamate, whereas D-***alanine*** hydroxamate perturbs the spectrum, but does not evoke the peak at 564 nm. In contrast, hydroxamates of L-valine and L-leucine in concns. equimolar to that of the enzyme produce only faint indications of change in the spectrum, but the hydroxamates of several other L-amino acids perturb the spectrum essentially independently of the identity of the side chain and in a qual. different manner from that of D-valine hydroxamate and D-leucine hydroxamate. At the high enzyme:substrate ratios used in the spectra expts., L-leucine hydroxamate and L-valine hydroxamate are rapidly hydrolyzed, hence their inability to perturb the spectrum of the Co substituted enzyme during the time course of a spectral expt. Values of kcat (catalytic const.) for L-amino acid hydroxamates, all of which are good reversible inhibitors of the hydrolysis of L-leucine-p-nitroanilide by ***Aeromonas*** ***aminopeptidase*** , ranged 0.01-5.6 min-1 for the native enzyme and 0.27-108 min-1 for the Co-substituted enzyme; their km values toward the Co aminopeptidase ranged 1.2 .times. 10-7 to 1.9 .times. 10-5 M. The mutual exclusivity of binding for hydroxamate inhibitors and 1-butaneboronic acid, previously shown by kinetics, was reflected in the characteristic spectra produced by these 2 types of inhibitors.

L5 ANSWER 3 OF 7 CAPLUS COPYRIGHT 2001 ACS DUPLICATE 4
AN 1986:621678 CAPLUS
DN 105:221678
TI Modified activity of Aeromonas aminopeptidase: metal ion substitutions and role of substrates
AU Bayliss, Mary E.; Prescott, John M.
CS Coll. Med., Texas A and M Univ., College Station, TX, 77843, USA
SO Biochemistry (***1986***), 25(24), 8113-17
CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
AB ***Aeromonas*** proteolytica ***Aminopeptidase*** (I) contains 2 nonidentical metal-binding sites that previously have been shown by both spectroscopy and kinetics to be capable of interacting with one another. The effects of metal ion substitutions on the susceptibility of the p-nitroanilides of L- ***alanine*** , L-valine, and L-leucine, substrates that are hydrolyzed at widely differing rates by native I, were studied by detg. values of the catalytic const. (kcat) and Km for the 16 metalloenzymes that resulted from all possible combinations of Zn2+, Co2+, Ni2+, and Cu2+ in each of the 2 sites. The different combinations of metal ions and substrates yielded a broad range in kinetic values; the kcat varied by >1800-fold, the Km by 3000-fold, and the kcat/Km ratios by >10,000. L-Leucine-p-nitroanilide was by far the most susceptible of the 3 substrates, and the hyperactivation previously obsd. with I contg. either Ni2+ or Cu2+ in the 1st binding site and Zn2+ in the 2nd site occurred only with the 2 poorer substrates, L- ***alanine*** -p-nitroanilide and L-valine-p-nitroanilide. Although I with Zn2+ in both sites hydrolyzed the substrates with N-terminal ***alanine*** and valine poorly, it was extremely effective toward L-leucine-p-nitroanilide. Neither metal-binding site could be identified as controlling either Km or kcat; both parameters were influenced by the identity of the metal ions, by the site each occupied, and, most strongly, by the substrate. The presence of Zn2+ in the 1st site generally resulted in high Km values in comparison with the other metalloenzymes and produced high kcat values toward both substrates with branched side-chains, whereas Cu2+ in the 1st site yielded low Km values with the 2 poorer substrates. A time dependence of activation occurred with metalloenzymes that had Cu2+ in the 1st site and another metal ion in the 2nd binding site, but was not obsd.

for any other combination of ions tested.

L5 ANSWER 4 OF 7 CAPLUS COPYRIGHT 2001 ACS
AN 1997:502427 CAPLUS
DN 127:118855
TI Purification and properties of an aminopeptidase from a protamine-degrading marine bacterium
AU Obata, Hitoshi; Sugiyama, Atsushi; Kawahara, Hidehisa; Muramatsu, Tsuyoshi
CS Dep. Biotechnol., Fac. Eng., Kansai Univ., Suita, 564, Japan
SO Biosci., Biotechnol., Biochem. (***1997***), 61(7), 1102-1108
CODEN: BBBIEJ; ISSN: 0916-8451
PB Japan Society for Bioscience, Biotechnology, and Agrochemistry
DT Journal
LA English
AB A protamine-degrading marine bacterium was isolated from marine soil and identified as Aeromonas salmonicida subsp. based on its taxonomic characteristics. An alanine-specific aminopeptidase, called aminopeptidase K, from an ext. of the strain was purified and characterized. Aminopeptidase K was purified .apprx.80-fold by fractionation with (NH4)2SO4 and column chromatog. on QA-52 cellulose, phenyl-Superose, and Superose 12. The purified enzyme was composed of 6 subunits of 86 kDa with a mol. wt. of 520 kDa according to gel filtration and SDS-PAGE. The N-terminal sequence of the enzyme was detd. The enzyme was inhibited by monoiodoacetate, N-ethylmaleimide, and puromycin. The Km and Vmax values were, resp., 0.28 mM and 49.4 .mu.mol/min/mg for L-Ala-.beta.-naphthylamide.. The optimum pH and temp. were 6.5 and 45.degree., resp. The purified enzyme was highly specific for L-Ala-.beta.-naphthylamide.

L5 ANSWER 5 OF 7 CAPLUS COPYRIGHT 2001 ACS
AN 1997:132825 CAPLUS
DN 126:185161
TI Debittering of Protein Hydrolyzates Using Aeromonas caviae Aminopeptidase
AU Izawa, Noboru; Tokuyasu, Ken; Hayashi, Kiyoshi
CS National Food Research Institute, Tsukuba, 305, Japan
SO J. Agric. Food Chem. (***1997***), 45(3), 543-545
CODEN: JAFCAU; ISSN: 0021-8561
PB American Chemical Society
DT Journal
LA English
AB The bitter-tasting peptide solns. prepd. from the protease hydrolyzate of milk casein and soy protein were treated with aminopeptidase produced by Aeromonas caviae T-64. The bitterness of these solns. were significantly reduced with an increase in the amt. of released free amino acids. Hydrophobic amino acids having values more than 1500 cal/mol, such as valine, isoleucine, leucine, tyrosine, and phenylalanine, accounted for more than 76% of the free amino acids released by the aminopeptidase. The results suggest that the enzyme hydrolyzed bitter peptides contg. hydrophobic amino acids in the N-terminal region and the bitterness of the peptides were reduced by removal of these amino acids.

L5 ANSWER 6 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 2
AN 1990:469068 BIOSIS
DN BA90:108488
TI A MEMBRANE-BOUND ALANINE AMINOPEPTIDASE FROM ACINETOBACTER-CALCOACETICUS
3. INHIBITION OF THE ENZYME.
AU JAHREIS G; AURICH H
CS INST. BIOCHEM., BEREICH MED., MARTIN-LUTHER-UNIV. HALLE-WITTENBERG, PSF 184, HALLE 4010, E. GER.
SO BIOMED BIOCHIM ACTA, (1990) 49 (5), 339-346.
CODEN: BBIADT. ISSN: 0232-766X.
FS BA; OLD
LA German
AB The ***alanine*** aminopeptidase from Acinetobacter calcoaceticus is inhibited by SH-reagents like p-hydroxymercuribenzoate, Ellman's reagent, N-bromosuccinimide, and metal chelating agents like 1,10-phenanthroline. The AAP is competitively inhibited by L-amino acids such as leucine, phenylalanine, and valine having hydrophobic side chains. Bacitracin (Ki = 2.0 .cntdot. 10-6 mol/l) inhibits AAP stronger than puromycin (Ki = 8.0 .cntdot. 10-6 mol/l). In contrast, the ***Aeromonas*** ***aminopeptidase*** (EC 3.4.11.10) is stronger inhibited by bestatin (Ki = 1.8 .cntdot. 10-8 mol/l) than the membrane-bound AAP from Acinetobacter-calcoaceticus. However, the binding of bestatin by both membrane-bound enzymes, Acinetobacter-APP and microsomal aminopeptidase M (EC 3.4.11.2), with Ki values of 8 .cntdot. 10-6 mol/l is in the same range.

L5 ANSWER 7 OF 7 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
AN 1996-02264 BIOTECHDS
TI Aminopeptidase and the production; enzyme production by Aeromonas salmonicida, and purification, and characterization
PA Daiwa-Chem.
LO Japan.
PI JP 07289256 ***7 Nov 1995***
AI JP 1994-83358 21 Apr 1994
PRAI JP 1994-83358 21 Apr 1994
DT Patent
LA Japanese
OS WPI: 1996-015262 [02]

AB A new aminopeptidase has the following physicochemical properties, it has an optimum activity at pH 6.5, it is stable at pH 7.0-10.0 at 4 deg for 5 hr, it has an optimum activity at 45 deg, it is stable up to 40 deg at pH 7.0 for 10 min, it has a high substrate specificity to an L- ***alanine*** residue, and it has a mol.wt. of 86,000 (SDS-PAGE). Also claimed are: (1) a method for the production of the ***aminopeptidase*** in which an ***Aeromonas*** sp. is cultured and the enzyme is isolated from the culture medium; and (2) Aeromonas salmonicida subsp. KUPD-1 (FERM P-14260) producing the aminopeptidase. The enzyme may be used to improve the taste an flavor of stored edible meat. In an example, A. salmonicida KUPD-1 was cultured in 20 ml of L-medium at 30 deg for 24 hr, and then for another 20 hr at 30 deg. 200 ml Of the culture was added to 20 l of a culture medium containing 0.2 g K2HPO4, 0.4 g Na2HPO4, 1.0 g NaCl, 0.2 g glucose and 0.5 g protamine in 100 ml water at 30 deg or 43 hr. The enzyme was purified by anion-exchange chromatography, hydrophobic chromatography, and gel filtration chromatography, to yield an active fraction with a specific activity of 29.9 U. (10pp)

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=> index bioscience
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SINCE FILE      TOTAL

ENTRY    SESSION
FULL ESTIMATED COST
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       BIOCOMMERCE, BIOSIS, BIOTECHABS,
BIOTECHDS, BIOTECHNO, CABA, CANCERLIT,
       CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI,
CROPB, CROPU, DDFB, DDFU, DGENE,
       DRUGB, DRUGLAUNCH, DRUGMONOG2, DRUGNL,
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          7   FILE USPATFULL
          1   FILE WPIDS
  58 FILES SEARCHED...
          1   FILE WPINDEX

  16 FILES HAVE ONE OR MORE ANSWERS,   59
FILES SEARCHED IN STNINDEX

L1   QUE (AEROMONAS(S)
AMINOPEPTIDASE)(L)(ALANINE OR ALANYL) AND
PY<2000

=> d rank
F1            7   USPATFULL
F2            5   BIOSIS
F3            5   CAPLUS
F4            5   MEDLINE
F5            4   LIFESCI
F6            3   EMBASE
F7            2   SCISEARCH
F8            1   AQUASCI
F9            1   BIOTECHABS
F10           1   BIOTECHDS
F11           1   BIOTECHNO
F12           1   ESBIOBASE
F13           1   JICST-EPLUS
F14           1   PASCAL
F15           1   WPIDS
F16           1   WPINDEX


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COST IN U.S. DOLLARS
SINCE FILE      TOTAL

ENTRY    SESSION
FULL ESTIMATED COST
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   3 FILES SEARCHED...
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  11 FILES SEARCHED...
  12 FILES SEARCHED...
L2   31 L1

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3   7 DUP REM L2 (24 DUPLICATES REMOVED)
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                ANSWER '6' FROM FILE CAPLUS
                ANSWER '7' FROM FILE BIOTECHDS

=> d bib ab 1-7

L3 ANSWER 1 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 1
AN 1999:8169 BIOSIS
DN PREV199900008169
TI Inhibition of Streptomyces griseus aminopeptidase and effects of calcium
    ions on catalysis and binding: Comparisons with the homologous enzyme
    Aeromonas proteolytica aminopeptidase.
AU Papir, Galia; Spungin-Bialik, Anya; Ben-Meir, Daniella; Fudim, Ella;
    Gilboa, Rotem; Greenblatt, Harry M.; Shoham, Gil; Lessel, Uta; Schomburg,
    Dietmar; Ashkenazi, Ruth; Blumberg, Shmaryahu (1)
CS (1) Sackler Inst. Molecular Med., Dep. Human Genetics Mol. Med., Sackler
    Fac. Med., Tel Aviv Univ., IL-69978 Tel Aviv Israel
SO European Journal of Biochemistry, (***Dec., 1998***) Vol. 258, No. 2,
    pp. 313-319.
    ISSN: 0014-2956.
DT Article
LA English
AB Streptomyces griseus ***aminopeptidase*** is a zinc metalloenzyme
    containing 2 mol zinc/mol protein, similar to the homologous enzyme
    Aeromonas proteolytica ***aminopeptidase*** . In addition, a
    unique Ca2+binding site has been identified in the Streptomyces enzyme,
    which is absent in the ***Aeromonas*** enzyme. Binding of Ca2+
    enhances stability of the Streptomyces enzyme and modulates its activity
    and affinity towards substrates and inhibitors in a structure-dependent
    manner. Among the three hydrophobic 4-nitroanilides of ***alanine*** ,
    valine and leucine, the latter displays the largest overall activation
    (increase in kcat/Km). Large enhancements in affinity (1/Ki) upon Ca2+
    binding have been observed for inhibitors with flexible (leucine-like)
    residues at their N-termini and smaller enhancements for inhibitors with
    rigid (phenylalanine-like) residues.

L3 ANSWER 2 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 2
AN 1997:460603 BIOSIS
DN PREV199799759806
TI Purification and properties of an aminopeptidase from a
    protamine-degrading marine bacterium.
AU Obata, Hitoshi (1); Sugiyama, Atsushi; Kawahara, Hidehisa; Muramatsu,
    Tsuyoshi
CS (1) Dep. Biotechnology, Fac. Eng., Kansai Univ., Yamatecho 3-3-35,
    Suita-shi, Osaka 564 Japan
SO Bioscience Biotechnology and Biochemistry, (1997) Vol. 61, No. 7, pp.
    1102-1108.
    ISSN: 0916-8451.
DT Article
LA English
AB A protamine-degrading marine bacterium was isolated from marine soil and
    identified as ***Aeromonas*** salmonicida subsp. based on its
    taxonomical characteristics. An ***alanine*** -specific
    aminopeptidase , called ***aminopeptidase*** K, from an extract
    of the strain was purified and characterized. The ***aminopeptidase***
    K was purified about 80-fold by fractionation with ammonium sulfate and
    column chromatography on QA-52 cellulose, Phenyl Superose and Superose 12.
    The purified enzyme is composed of 6 subunits of 86 kDa with a molecular
    mass of 520 kDa according to gel filtration and SDS-PAGE. The N-terminal
    sequence of the enzyme was H cntdot Gly-Gln-Gln-Pro-Gln-Ile-Lys-Try-Tyr-

His-Asp-Tyr-Asp-Ala-Pro-Asp-Tyr-Tyr-Ile-Thr-. It is inhibited by monoiodoacetate, N-ethylmaleimide, and puromycin. The Michaelis constant (K-m) and the maximal rate of hydrolysis (V-max) were, respectively, 0.28 mM and 49.4 mu-mol/min/mg for the L-Ala-beta-naphthylamide substrate. The optimum pH and optimum temperature were 6.5 and 45 degree C, respectively. The purified enzyme was highly specific to L-Ala-beta-naphthylamide.

L3 ANSWER 3 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 4
AN 1990:469068 BIOSIS
DN BA90:108488
TI A MEMBRANE-BOUND ALANINE AMINOPEPTIDASE FROM ACINETOBACTER-CALCOACETICUS 3. INHIBITION OF THE ENZYME.
AU JAHREIS G; AURICH H
CS INST. BIOCHEM., BEREICH MED., MARTIN-LUTHER-UNIV. HALLE-WITTENBERG, PSF 184, HALLE 4010, E. GER.
SO BIOMED BIOCHIM ACTA, (1990) 49 (5), 339-346.
CODEN: BBIADT. ISSN: 0232-766X.
FS BA; OLD
LA German
AB The ***alanine*** ***aminopeptidase*** from Acinetobacter calcoaceticus is inhibited by SH-reagents like p-hydroxymercuribenzoate, Ellman's reagent, N-bromosuccinimide, and metal chelating agents like 1,10-phenanthroline. The AAP is competitively inhibited by L-amino acids such as leucine, phenylalanine, and valine having hydrophobic side chains. Bacitracin (Ki = 2.0 .cntdot. 10-6 mol/l) inhibits AAP stronger than puromycin (Ki = 8.0 .cntdot. 10-6 mol/l). In contrast, the ***Aeromonas*** ***aminopeptidase*** (EC 3.4.11.10) is stronger inhibited by bestatin (Ki = 1.8 .cntdot. 10-8 mol/l) than the membrane-bound AAP from Acinetobacter-calcoaceticus. However, the binding of bestatin by both membrane-bound enzymes, Acinetobacter-APP and *microsomal* ***aminopeptidase*** M (EC 3.4.11.2), with Ki values of 8 .cntdot. 10-6 mol/l is in the same range.

L3 ANSWER 4 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 5
AN 1987:383831 BIOSIS
DN BA84:70328
TI HYDROXAMATE-INDUCED SPECTRAL PERTURBATIONS OF COBALT AEROMONAS AMINOPEPTIDASE.
AU WILKES S H; PRESCOTT J M
CS INST. OCCUPATIONAL MED., COLL. MED., TEXAS A AND M UNIV., COLLEGE STATION, TEX. 77843.
SO J BIOL CHEM, (1987) 262 (18), 8621-8625.
CODEN: JBCHA3. ISSN: 0021-9258.
FS BA; OLD
LA English
AB The absorption spectrum of cobalt(II)-substituted ***Aeromonas*** ***aminopeptidase*** is markedly perturbed by the presence of equimolar concentrations of D-amino acid hydroxamates and acyl hydroxamates that have previously been shown to be powerful inhibitors of this enzyme (Wilkes, S.H., and Prescott, J.M. (1983) J. Biol. Chem. 258, 13517-13521). D-Valine hydroxamate produces the most distinctive perturbation, splitting the characteristic 527 nm absorption peak of the cobalt enzyme to form peaks at 564, 520, and 487 nm with molar extinction values of 126, 98, and 67 M-1 cm-1, respectively. A qualitatively similar pertubation, albeit with lower extinction values, results from the addition of D-leucine hydroxamate, whereas D- ***alanine*** hydroxamate perturbs the spectrum but does not evoke the peak at 564 nm. In contrast, hydroxamates of L-valine and L-leucine in concentrations equimolar to that of the enzyme produce only faint indications of change in the spectrum, but the hydroxamates of several other L-amino acids perturb the spectrum essentially independently of the identity of the side chain and in a qualitatively different manner from that of D-valine hydroxamate and D-leucine hydroxamate. At the high enzyme:substrate ratios used in the spectral experiments, L-leucine hydroxamate and L-valine hydroxamate proved to be rapidly hydrolyzed, hence their inability to perturb the spectrum of the cobalt-substituted enzyme during the time course of a spectral experiment. Values of kcat for L-amino acid hydroxamates, all of which are good reversible inhibitors of the hydrolysis of L-leucine-p-nitroanilide by ***Aeromonas*** ***aminopeptidase***, were found to range from 0.01 min-1 to 5.6 min-1 for the native enzyme and from 0.27 min-1 to 108 min-1 for the cobalt-substituted enzyme; their km values toward the cobalt ***aminopeptidase*** range from 1.2 .times. 10-7 M to 1.9 .times. 10-5 M. The mutual exclusivity of binding for hydroxamate inhibitors and 1-butaneboronic acid, previously shown by kinetics (Baker, J.O., Wilkes, S.H., Bayliss, M.E., and Prescott, J.M. (1983) Biochemistry 22,2098-2103), was reflected in the characteristic spectra produced by these two types of inhibitors.

L3 ANSWER 5 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 6
AN 1987:109472 BIOSIS
DN BA83:58450
TI MODIFIED ACTIVITY OF AEROMONAS AMINOPEPTIDASE METAL ION SUBSTITUTIONS AND

ROLE OF SUBSTRATES.
AU BAYLISS M E; PRESCOTT J M
CS INST. OCCUPATIONAL MED., COLL. MED., TEXAS A AND M UNIV., COLLEGE STATION, TEX. 77843.
SO BIOCHEMISTRY, (1986) 25 (24), 8113-8117. CODEN: BICHAW. ISSN: 0006-2960.
FS BA; OLD
LA English
AB ***Aeromonas*** ***aminopeptidase*** contains two nonidentical metal binding sites that have been shown by both spectroscopy and kinetics to be capable of interacting with one another [Prescott, J. M., Wagner, F. W., Holmquist, B., & Vallee, B. L. (1985) Biochemistry 24, 5350-5356]. The effects of metal ion substitutions on the susceptibility of the p-nitroanilides of L- ***alanine*** , L-valine, and L-leucine-substrates that are hydrolyzed at widely differing rates by native ***Aeromonas*** ***aminopeptidase*** -were studied by determining values of kcat and Km for the 16 metalloenzymes that result from all possible combinations of Zn2+, Co2+, Ni2+, and Cu2+ in each of the two sites. The different combinations of metal ions and substrates yield a broad range in kinetic values; kcat varies by more than 1800-fold, Km by 3000-fold, and kcat/Km ratios by more than 10,000. L-Leucine-p-nitroanilide is by far the most suceptible of the three substrates, and the hyperactivation previously observed with ***aminopeptidase*** containing either Ni2+ or Cu2+ in the first binding site and Zn2+ in the second site occurs only with the two poorer substrates, L- ***alanine*** -p-nitroanilide and L-valine-p-nitroanilide. Although the enzyme with Zn2+ in both sites hydrolyzes the substrates with N-terminal ***alanine*** and valine poorly, it is extremely effective toward L-leucin-p-nitroanilide. Neither metal binding site can be identified as controlling either Km or kcat; both parameters are influenced by the identity of the metal ions, by the site each ocupies, and, most strongly, by the substrate. The presence of Zn2+ in the first site generally results in high Km values in comparison with the other metalloenzymes and produces high kcat values toward both substrates with branched side chains, whereas Cu2+ in the first site yields low Km values with the two poorer substrates. A time dependence of activation occurs with metalloenzymes that have Cu2+ in the first site and another metal ion in the second binding site, but was not observed for any other combination of ions tested.

L3 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2001 ACS
AN 1997:132825 CAPLUS
DN 126:185161
TI Debittering of Protein Hydrolyzates Using Aeromonas caviae Aminopeptidase
AU Izawa, Noboru; Tokuyasu, Ken; Hayashi, Kiyoshi
CS National Food Research Institute, Tsukuba, 305, Japan
SO J. Agric. Food Chem. (***1997***), 45(3), 543-545
CODEN: JAFCAU; ISSN: 0021-8561
PB American Chemical Society
DT Journal
LA English
AB The bitter-tasting peptide solns. prepd. from the protease hydrolyzate of milk casein and soy protein were treated with aminopeptidase produced by *Aeromonas caviae* T-64. The bitterness of these solns. were significantly reduced with an increase in the amt. of released free amino acids. Hydrophobic amino acids having values more than 1500 cal/mol, such as valine, isoleucine, leucine, tyrosine, and phenylalanine, accounted for more than 76% of the free amino acids released by the aminopeptidase. The results suggest that the enzyme hydrolyzed bitter peptides contg. hydrophobic amino acids in the N-terminal region and the bitterness of the peptides were reduced by removal of these amino acids.

L3 ANSWER 7 OF 7 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
AN 1996-02264 BIOTECHDS
TI Aminopeptidase and the production; enzyme production by Aeromonas salmonicida, and purification, and characterization
PA Daiwa-Chem.
LO Japan.
PI JP 07289256 ***7 Nov 1995***
AI JP 1994-83358 21 Apr 1994
PRAI JP 1994-83358 21 Apr 1994
DT Patent
LA Japanese
OS WPI: 1996-015262 [02]
AB A new ***aminopeptidase*** has the following physicochemical properties, it has an optimum activity at pH 6.5, it is stable at pH 7.0-10.0 at 4 deg for 5 hr, it has an optimum activity at 45 deg, it is stable up to 40 deg at pH 7.0 for 10 min, it has a high substrate specificity to an L- ***alanine*** residue, and it has a mol.wt. of 86,000 (SDS-PAGE). Also claimed are: (1) a method for the production of the ***aminopeptidase*** in which an ***Aeromonas*** sp. is cultured and the enzyme is isolated from the culture medium; and (2) ***Aeromonas*** salmonicida subsp. KUPD-1 (FERM P-14260) producing the ***aminopeptidase*** . The enzyme may be used to improve the taste an

flavor of stored edible meat. In an example, A. salmonicida KUPD-1 was cultured in 20 ml of L-medium at 30 deg for 24 hr, and then for another 20 hr at 30 deg. 200 ml Of the culture was added to 20 l of a culture medium containing 0.2 g K2HPO4, 0.4 g Na2HPO4, 1.0 g NaCl, 0.2 g glucose and 0.5 g protamine in 100 ml water at 30 deg or 43 hr. The enzyme was purified by anion-exchange chromatography, hydrophobic chromatography, and gel filtration chromatography, to yield an active fraction with a specific activity of 29.9 U. (10pp)

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